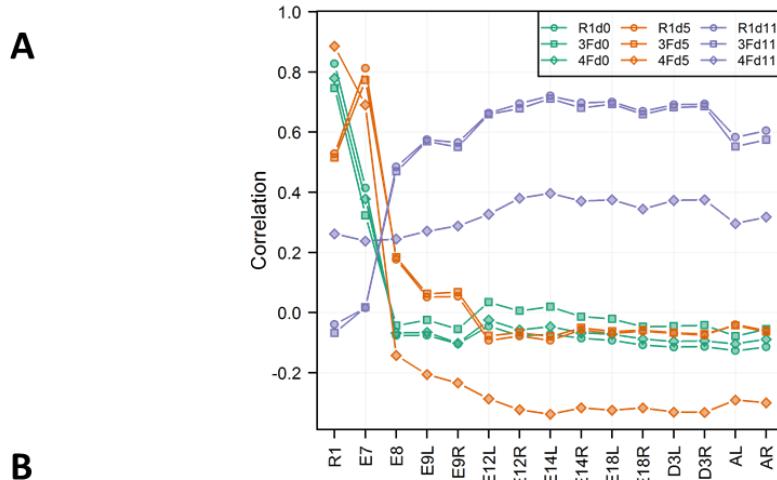


SUPPLEMENTAL MATERIAL

SUPPLEMENTARY FIGURES and LEGENDS



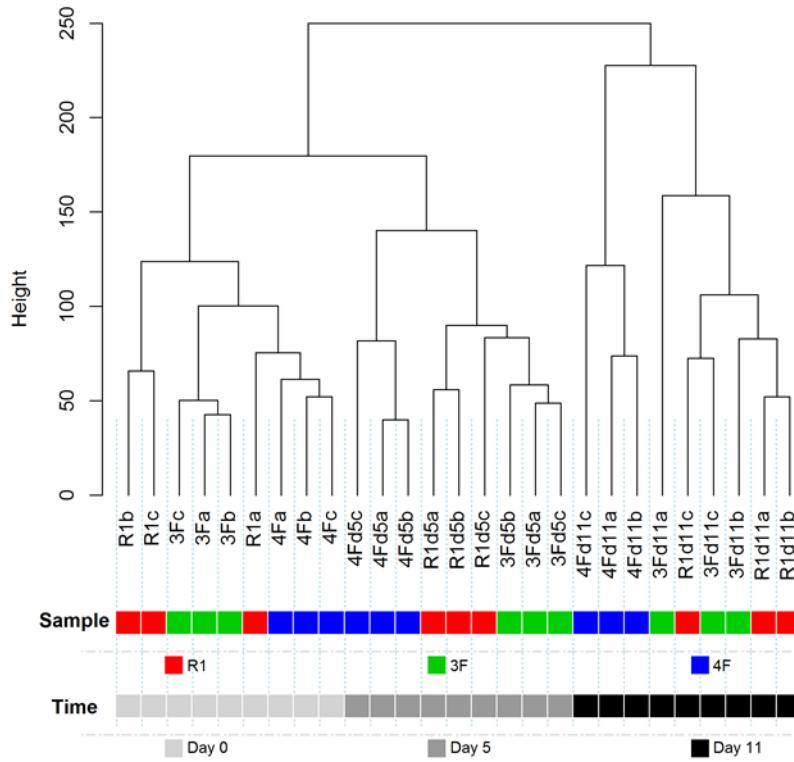
B

	R1d0	3Fd0	4Fd0	R1d5	3Fd5	4Fd5	R1d11	3Fd11	4Fd11
R1	0.827402	0.746614	0.779053	0.528068	0.515298	0.885699	-0.03957	-0.06751	0.261984
E7	0.41459	0.323312	0.378211	0.812794	0.772942	0.69041	0.015126	0.017201	0.237908
E8	-0.07657	-0.04374	-0.06784	0.17712	0.183867	-0.14236	0.484842	0.469251	0.244693
E9L	-0.07509	-0.02479	-0.06566	0.051544	0.062139	-0.20608	0.574923	0.569248	0.270991
E9R	-0.10391	-0.05536	-0.10189	0.05355	0.068022	-0.23395	0.565332	0.550566	0.28819
E12L	-0.04534	0.034749	-0.02492	-0.09269	-0.07711	-0.28687	0.662953	0.659298	0.327199
E12R	-0.07712	0.005574	-0.05771	-0.0781	-0.06625	-0.32295	0.694961	0.678818	0.380548
E14L	-0.07258	0.019568	-0.04636	-0.09234	-0.07966	-0.33793	0.720497	0.711342	0.396678
E14R	-0.08511	-0.01372	-0.06737	-0.05777	-0.0507	-0.31688	0.697579	0.68057	0.37085
E18L	-0.09251	-0.021	-0.07186	-0.06951	-0.06262	-0.32451	0.700338	0.693054	0.375005
E18R	-0.10769	-0.04698	-0.08797	-0.06227	-0.05854	-0.31672	0.669179	0.659413	0.344603
D3L	-0.11489	-0.04534	-0.09604	-0.06941	-0.0666	-0.33097	0.69108	0.68234	0.372942
D3R	-0.11307	-0.04168	-0.09419	-0.07502	-0.0713	-0.33196	0.693841	0.685846	0.375249
AL	-0.12679	-0.0785	-0.10384	-0.03998	-0.04308	-0.29078	0.583283	0.552355	0.295987
AR	-0.11448	-0.05555	-0.08856	-0.0604	-0.0631	-0.30015	0.60483	0.574721	0.317862

C

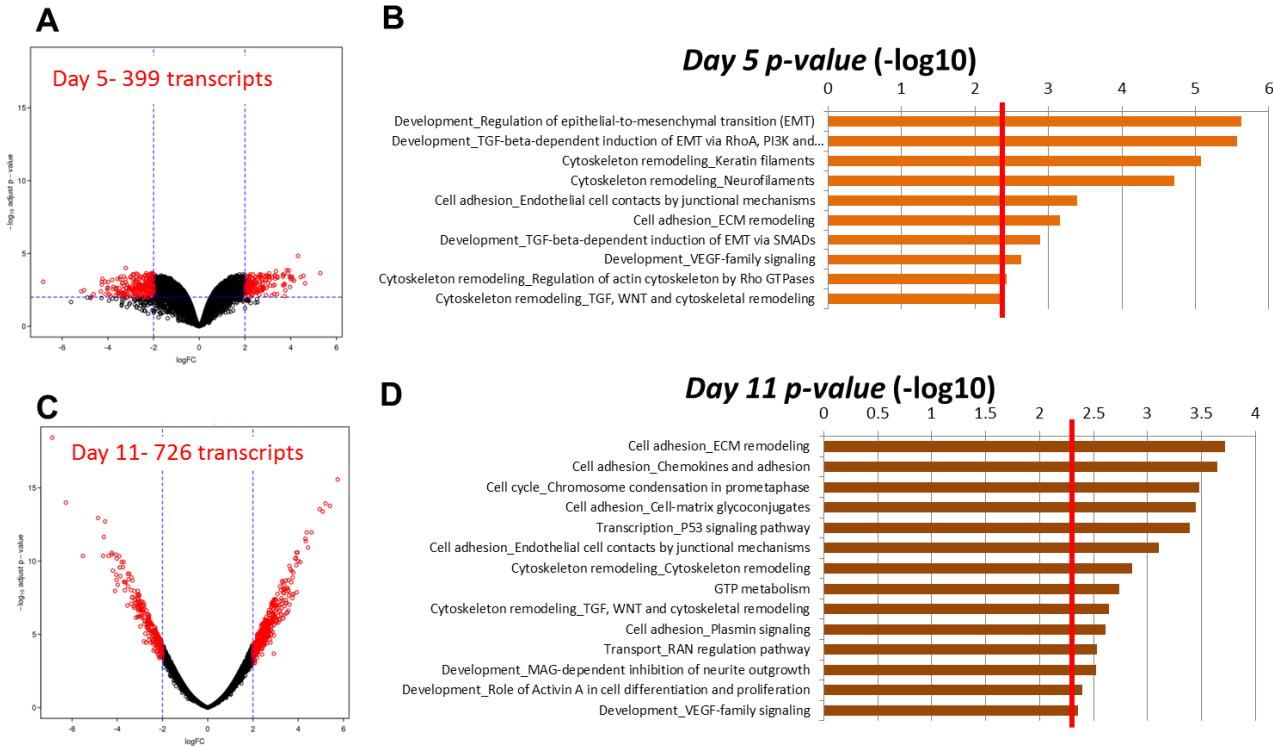
Supplementary Figure 1

Supplementary Figure 1. Correlation of pluripotent cell lines at various time points of differentiation to natural heart development roadmap. A. Correlation between three time points, day 0 (d0), d5 and d11 for each of the pluripotent cells (R1-ESC, R1; 3F-iPSC, 3F; 4F-iPSC, 4F) and stages of cardiac development (from embryonic day (E)7.5 to the adult). B. Pearson's correlation matrix used to generate panel A. C. Hierarchical clustering heatmap based on the Pearson's correlations between all samples. Gene expression for triplicate samples was averaged for the calculation of Pearson's correlation. Red color represents high correlation and green color is low correlation.



Supplementary Figure 2

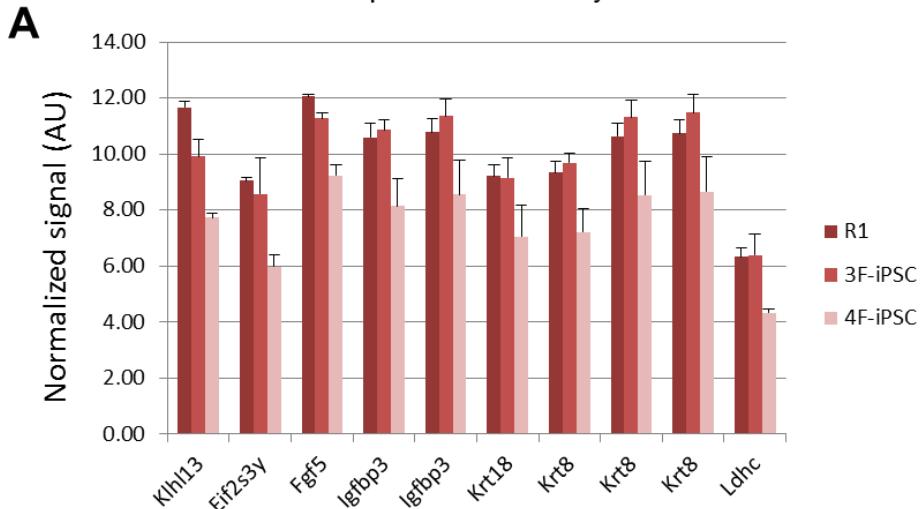
Supplementary Figure 2. Stem cells with differential cardiogenic profile cluster independently according to overall expressome. Unsupervised hierarchical clustering of pluripotent cells and their progeny based on complete gene expression profile. Separation of 4F-iPS in independent branches is apparent for day 5 and 11 of differentiation, while 3F-iPS and R1 ESC cluster together across the studied time frame.



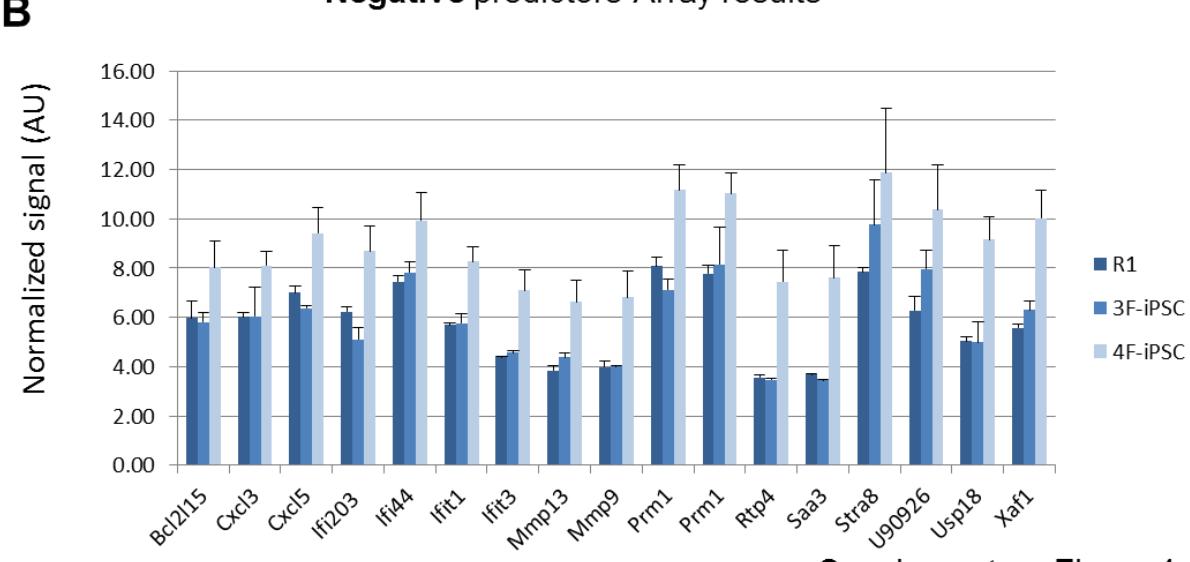
Supplementary Figure 3

Supplementary Figure 3. Biological functions underlying disruption of cardiogenicity across differentiation stages. Cardiogenic proficient (3F-iPS) and impaired (4F-iPS) cell progeny were compared at day 5 (A,B) and day 11 (C,D) of differentiation. Significant biological functions prioritized according to gene ontology analysis resulted in an increasing number of disrupted pathways responsible for the observed differences in phenotype. Red bar marks statistical significance p-value= 0.05.

Positive predictors-Array results

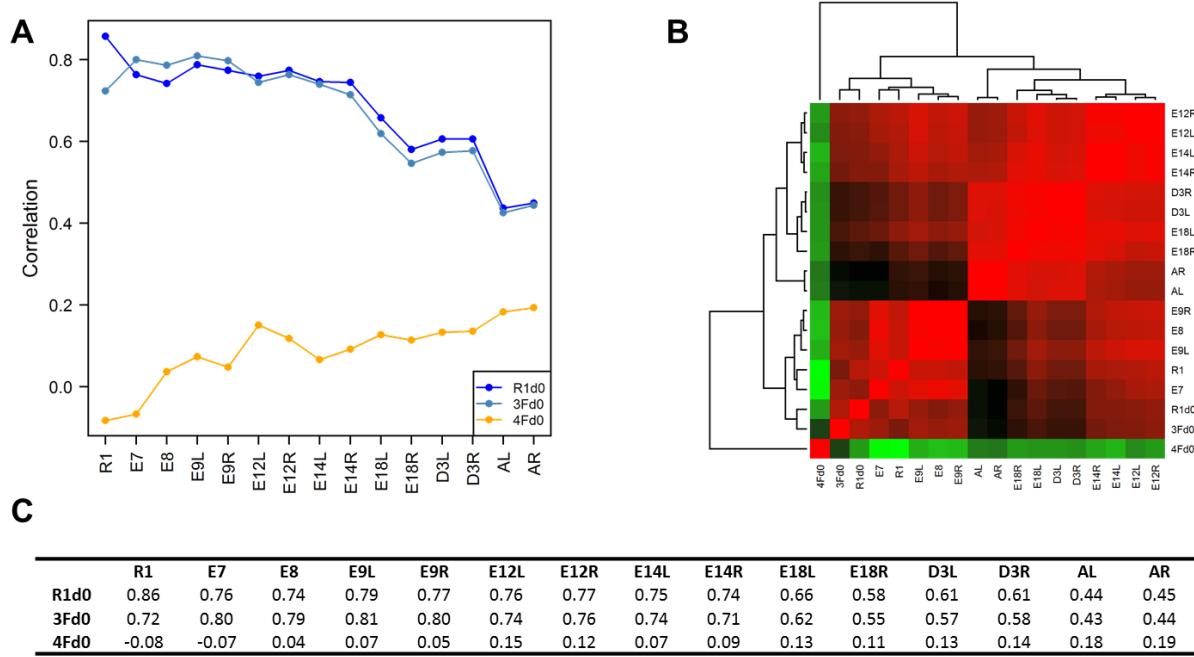


Negative predictors-Array results



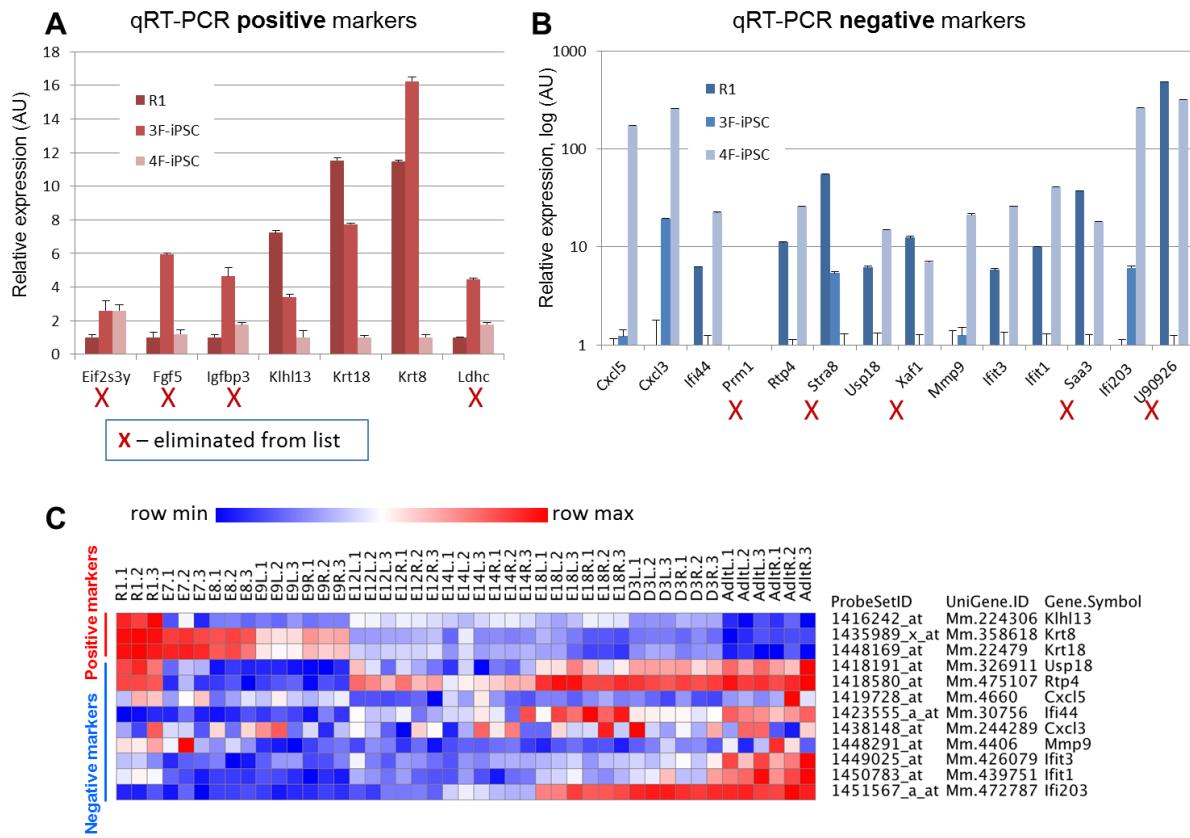
Supplementary Figure 4

Supplementary Figure 4. Expression profile unique to non-cardiogenic 4F-iPS according to microarray platform. Bioinformatic analysis of microarray data reveals a panel of 7 genes downregulated in 4F-iPS compared to 3F-iPS and R1-ESCs (A) as well as 14 genes showing higher expression values in 4F-iPS relative to 3F and ESCs. Those genes were used to create a predictive panel for downstream cardiogenicity of reprogrammed lines.



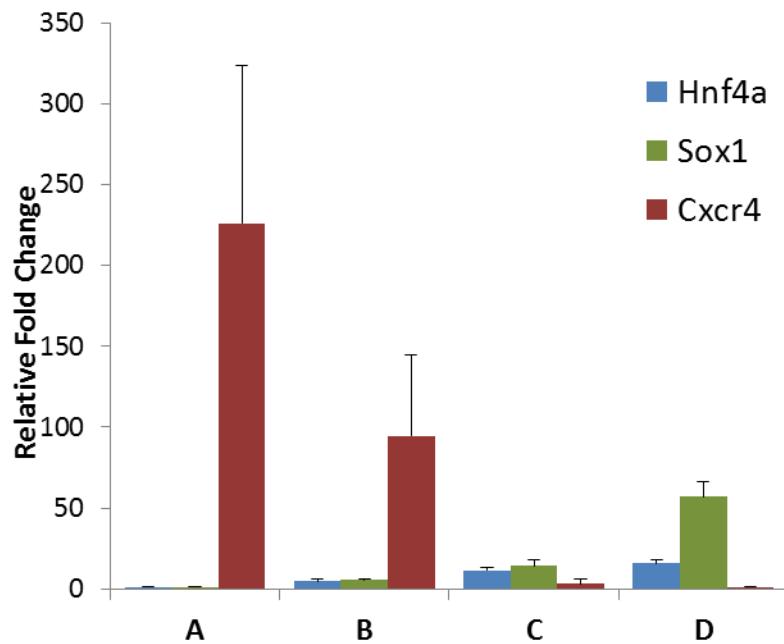
Supplementary Figure 5

Supplementary Figure 5. Correlation between pluripotent samples and heart development roadmap based on 23 genes uniquely regulated in low-cardiogenic 4F-iPSC. A. Correlation between R1-ESC (R1), 3F-iPSC (3F) and 4F-iPSC (4F) at day 0 (d0) and each of the embryonic stages included in the roadmap (E7.5 through adult) as resulting from Pearson's correlation analysis. B. Heatmap representing correlation between all the samples in both datasets. C. Pearson's correlation matrix with values used in panel A. Red color represents high correlation and green color is low correlation.



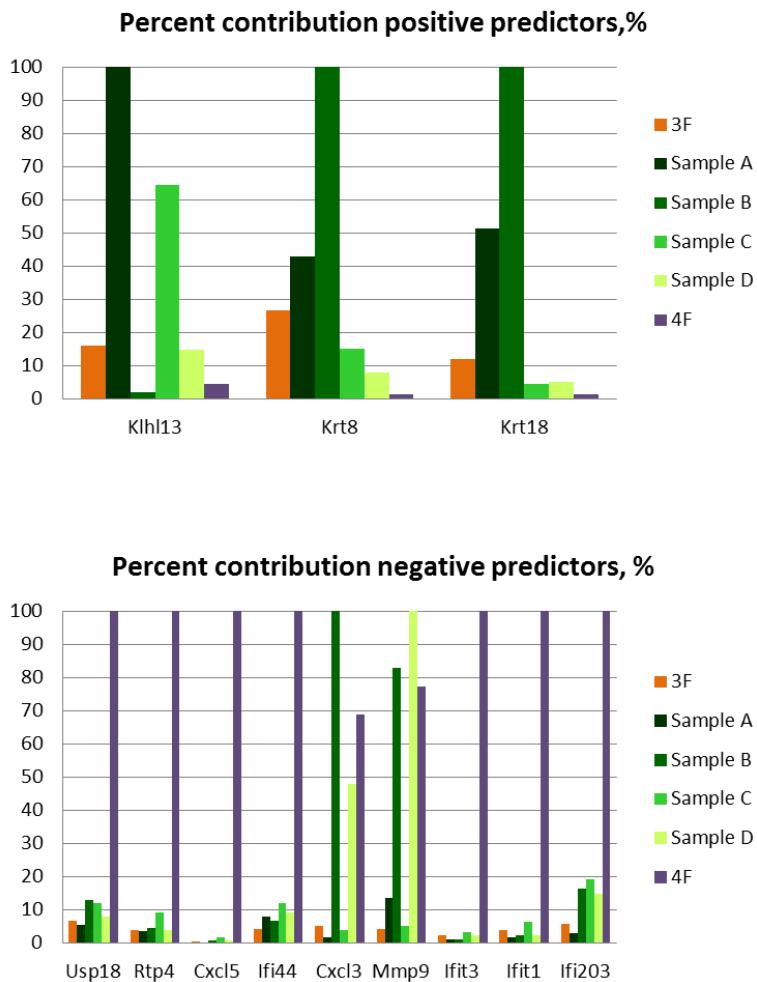
Supplementary Figure 6

Supplementary Figure 6. PCR validation of predictive genes. Expression profile based on qRT-PCR for 7 positive markers (A) and 14 negative markers (B). Red X marks genes that do not fulfill expression criteria based on PCR results. Expression matrix through natural cardiac development for the resulting 12 gene-panel differentially expressed in non-cardiogenic cells.



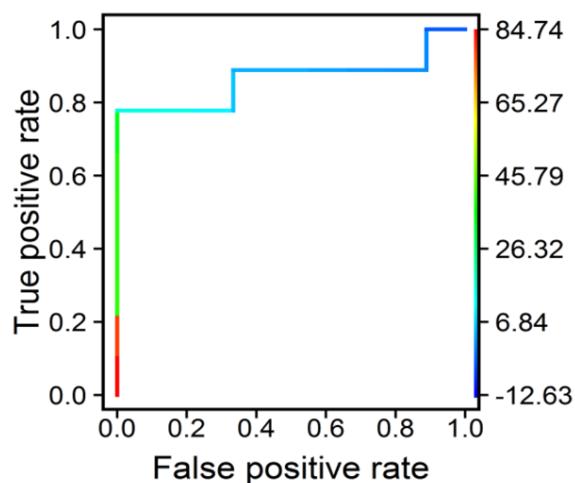
Supplementary Figure 7

Supplementary Figure 7. Relative expression levels of mesendoderm marker Cxcr4 in assayed reprogrammed lines at gastrulation stage. Relative expression values for mesendoderm (Cxcr4), endoderm (Hnf4a) and ectoderm (Sox1) markers in differentiating lines at gastrulation stage. Results are normalized to the lowest value for each gene.



Supplementary Figure 8

Supplementary Figure 8. Percentage expression of positive and negative predictor genes in reprogrammed lines. Percentage expression of predictive genes was calculated using highest relative expression for each gene as 100%. Plotted values were averaged into the average percentage expression of positive and negative predictors shown in figure 4D and 4E.

A**B**

Sample	Score	Label
LentiCF2	-12.6295	late (bad)
DoxMEF2	-3.9642	early (good)
LentiTTF1	0.732398	late (bad)
LentiMEF2	1.328292	late (bad)
LentiCF1	1.809688	late (bad)
LentiTTF3	2.935062	late (bad)
LentiCF3	3.959507	late (bad)
DoxMEF1	4.056655	early (good)
LentiMEF1	5.678349	late (bad)
LentiMEF3	10.58876	late (bad)
LentiTTF2	13.6569	late (bad)
DoxCF2	14.3467	early (good)
DoxTTF2	34.3157	early (good)
DoxTTF3	39.30864	early (good)
DoxCF3	39.81611	early (good)
DoxCF1	39.85845	early (good)
DoxMEF3	40.07461	early (good)
DoxTTF1	79.33098	early (good)

Supplementary Figure 9

Supplementary Figure 9. ROC curve analysis. A. ROC curve for true positive rate (TPR) versus false positive rate (FPR). Right y-axis shows color scale for score values with red representing higher values and blue lower. The curve is colored according to the score. B. Data used for ROC curve analysis.

Supplementary Table 1. Primers used for candidate gene-based qRT-PCR

	Gene Symbol	Primer
Positive predictors	Ldhc	Mm.PT.51.8763876
	Klhl13	Mm.PT.51.12521491
	Eif2s3y	Mm.PT.51.14046884
	Krt8	Mm.PT.51.16949649
	Fgf5	Mm.PT.51.6910518
	Krt18	Mm.PT.51.6818716
	Igfbp3	Mm.PT.51.11473386
Negative predictors	Usp18	Mm.PT.51.13216257
	Rtp4	Mm.PT.51.7878084
	Cxcl5	Mm.PT.51.6756000.g
	Stra8	Mm.PT.51.13386884.gs
	Ifi44	Mm.PT.51.8192586
	Cxcl3	Mm.PT.51.12834039.g
	Xaf1	Mm.PT.51.16665971
	Mmp9	Mm.PT.51.13590399.gs
	Ifit3	Mm.PT.51.21979271.g
	Ifit1	Mm.PT.51.17583238.g
	Saa3	Mm.PT.51.17505312.gs
	Ifi203 /// LOC100044071	Mm.PT.51.11911455.g
	U90926	Mm.PT.51.5324283

Supplementary Table 2. Panel of cardiogenesis-related genes

ID	UniGene ID	Gene Title	Gene Symbol	Entrez Gene	Pathway
1449425_at	Mm.33653	wingless-related MMTV integration site 2	Wnt2	22413	Wnt_Signaling // GenMAPP
1448818_at	Mm.28754 4	wingless-related MMTV integration site 5A	Wnt5a	22418	
1439373_x_a_t	Mm.32181 8	wingless-related MMTV integration site 5B	Wnt5b	22419	
1450763_x_a_t	Mm.15909 1	wingless-related MMTV integration site 3	Wnt3	22415	
1436791_at	Mm.28754 4	wingless-related MMTV integration site 5A	Wnt5a	22418	
1419301_at	Mm.86755	frizzled homolog 4 (Drosophila)	Fzd4	14366	
1449254_at	Mm.28847 4	secreted phosphoprotein 1	Spp1	20750	
1422213_s_a_t	Mm.42011	forkhead box H1	Foxh1	14106	TGF_Beta_Signaling_Pathway // GenMAPP
1437779_at	Mm.42011	forkhead box H1	Foxh1	14106	
1422771_at	Mm.32575 7	MAD homolog 6 (Drosophila)	Smad6	17130	
1422053_at	Mm.8042	inhibin beta-A	Inhba	16323	
1416081_at	Mm.22371 7	MAD homolog 1 (Drosophila)	Smad1	17125	
1426397_at	Mm.17234 6	transforming growth factor, beta receptor II	Tgfb2	21813	
1459843_s_a_t	Mm.22371 7	MAD homolog 1 (Drosophila)	Smad1	17125	
1448208_at	Mm.22371 7	MAD homolog 1 (Drosophila)	Smad1	17125	
1422754_at	Mm.24959 4	tropomodulin 1	Tmod1	21916	Striated_muscle_contraction // GenMAPP
1424967_x_a_t	Mm.24747 0	troponin T2, cardiac	Tnnt2	21956	
1450813_a_a_t	Mm.44379	troponin I, skeletal, slow 1	Tnni1	21952	
1418726_a_a_t	Mm.24747 0	troponin T2, cardiac	Tnnt2	21956	
1420693_at	Mm.4103	myomesin 1	Myom1	17929	
1448665_at	Mm.27560 8	dystrophin, muscular dystrophy	Dmd	13405	
1418370_at	Mm.43992 1	troponin C, cardiac/slow skeletal	Tnnc1	21924	
1425028_a_a_t	Mm.646	tropomyosin 2, beta	Tpm2	22004	Smooth_muscle_contraction // GenMAPP //
1417307_at	Mm.27560 8	dystrophin, muscular dystrophy	Dmd	13405	
1452670_at	Mm.27177 0	myosin, light polypeptide 9, regulatory	Myl9	98932	
1416454_s_a_t	Mm.21302 5	actin, alpha 2, smooth muscle, aorta	Acta2	11475	
1427768_s_a_t	Mm.7353	myosin, light polypeptide 3	Myl3	17897	
1454906_at	Mm.25931 8	retinoic acid receptor, beta	Rarb	218772	Nuclear_Receptors // GenMAPP
1427884_at	Mm.24955 5	collagen, type III, alpha 1	Col3a1	12825	
1450857_a_a_t	Mm.27779 2	collagen, type I, alpha 2	Col1a2	12843	
1427883_a_a_t	Mm.24955 5	collagen, type III, alpha 1	Col3a1	12825	
1423110_at	Mm.27779 2	collagen, type I, alpha 2	Col1a2	12843	
1446326_at	Mm.27779 2	collagen, type I, alpha 2	Col1a2	12843	
1416295_a_a_t	Mm.2923	interleukin 2 receptor, gamma chain	Il2rg	16186	
1455494_at	Mm.27773 5	collagen, type I, alpha 1	Col1a1	12842	Collagen-related genes
1423669_at	Mm.27773 5	collagen, type I, alpha 1	Col1a1	12842	

1434411_at	Mm.3819	collagen, type XII, alpha 1	Col12a1	12816	
1420941_at	Mm.20954	regulator of G-protein signaling 5	Rgs5	19737	Calcium Regulation in cardiac cells //
1417466_at	Mm.20954	regulator of G-protein signaling 5	Rgs5	19737	
1422673_at	Mm.13371_9	protein kinase D1	Prkd1	18760	
1447623_s_at	Mm.13371_9	protein kinase D1	Prkd1	18760	
1456307_s_at	Mm.28820_6	adenylate cyclase 7	Adcy7	11513	
1456475_s_at	Mm.47921_4	protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	19088	
1420859_at	Mm.3193	protein kinase inhibitor, alpha	Pkia	18767	
1422208_a_tt	Mm.17604	guanine nucleotide binding protein (G protein), beta 5	Gnb5	14697	
1439036_a_tt	Mm.4550	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	11931	
1424942_a_tt	Mm.2444	myelocytomatosis oncogene	Myc	17869	Reprogramming/Pluripotency
1429388_at	Mm.47808_0	Nanog homeobox	Nanog	71950	
1416967_at	Mm.65396	SRY-box containing gene 2	Sox2	20674	
1417945_at	Mm.17031	POU domain, class 5, transcription factor 1	Pou5f1	18999	
1420085_at	Mm.4956	fibroblast growth factor 4	Fgf4	14175	
1418351_a_tt	Mm.89772	DNA methyltransferase 3B	Dnmt3b	13436	
1424152_at	Mm.25691_6	sal-like 4 (Drosophila)	Sall4	99377	
1441914_x_tt	Mm.4947	Fibroblast growth factor 3	Fgf3	14174	Gastrulation
1449379_at	Mm.285	kinase insert domain protein receptor	Kdr	16542	
1421951_at	Mm.4965	LIM homeobox protein 1	Lhx1	16869	
1419304_at	Mm.913	brachyury	T	20997	
1417625_s_tt	Mm.6522	chemokine (C-X-C motif) receptor 7	Cxcr7	12778	
1448710_at	Mm.1401	chemokine (C-X-C motif) receptor 4	Cxcr4	12767	Precardiac
1425464_at	Mm.32928_7	GATA binding protein 6	Gata6	14465	
1450723_at	Mm.42242	ISL1 transcription factor, LIM/homeodomain	Isl1	16392	
1426557_at	Mm.1404	mesoderm posterior 1	Mesp1	17292	
1453351_at	Mm.31452	T-box 20	Tbx20	57246	
1425158_at	Mm.31452	T-box 20	Tbx20	57246	
1418863_at	Mm.24766_9	GATA binding protein 4	Gata4	14463	
1425995_s_tt	Mm.38933_9	Wilms tumor 1 homolog	Wt1	22431	
1417525_at	Mm.4746	heart and neural crest derivatives expressed transcript 1	Hand1	15110	
1418910_at	Mm.595	bone morphogenetic protein 7	Bmp7	12162	Endoderm
1429524_at	Mm.42019	myosin IF	Myoif	17916	
1420512_at	Mm.10359_3	dickkopf homolog 2 (Xenopus laevis)	Dkk2	56811	
1421657_a_tt	Mm.27910_3	SRY-box containing gene 17	Sox17	20671	
1429177_x_tt	Mm.27910_3	SRY-box containing gene 17	Sox17	20671	

Supplementary Table 3. Differentially expressed transcripts between undifferentiated 3F- and 4F-iPSC

ProbesetIDs	UniGene ID	Gene Symbol	H9a	H9b	H9c	BLa	BLb	BLc	logFC	adj.P.Val
1425137_a_at	Mm.88795	H2-Q10	8.29	8.64	8.58	5.08	5.49	5.58	-3.13	3.23E-11
1428750_at	Mm.195932	Cdc42ep2	10.15	9.98	9.85	6.91	7.04	6.74	-3.10	1.62E-11
1416561_at	Mm.272120	Gad1	8.19	8.30	8.29	5.51	5.96	4.63	-2.90	1.03E-08
1420647_a_at	Mm.358618	Krt8	12.84	10.86	10.76	8.83	8.32	8.82	-2.83	3.70E-06
1436419_a_at	Mm.372315	1700097N02Rik	13.06	12.98	13.07	10.37	10.90	9.41	-2.81	4.52E-08
1435989_x_at	Mm.358618	Krt8	12.63	10.76	10.66	8.64	8.48	8.57	-2.79	2.25E-06
1423323_at	Mm.439913	Tacstd2	7.23	6.47	7.23	3.92	4.17	4.50	-2.78	2.63E-09
1423691_x_at	Mm.358618	Krt8	12.68	10.64	10.61	8.57	8.51	8.52	-2.78	4.02E-06
1423062_at	Mm.29254	Igfbp3	11.69	10.22	10.69	7.77	8.10	8.57	-2.72	2.45E-07
1455692_x_at	Mm.372315	1700097N02Rik	12.90	12.66	12.79	10.22	10.85	9.24	-2.68	2.16E-07
1417156_at	Mm.439699	Krt19	9.93	8.28	8.40	6.40	6.19	6.04	-2.66	6.86E-07
1449335_at	Mm.4871	Timp3	11.65	11.14	12.47	9.83	8.48	9.16	-2.60	1.15E-06
1438883_at	Mm.5055	Fgf5	8.60	8.45	8.66	5.67	5.91	6.37	-2.59	1.43E-09
1439483_at	---	AI506816	8.42	8.16	8.53	6.10	5.49	5.89	-2.54	1.45E-09
1448194_a_at	Mm.14802	H19	10.77	10.50	10.68	8.85	7.26	8.25	-2.53	4.19E-07
1458268_s_at	Mm.29254	Igfbp3	10.49	9.06	9.49	7.12	7.20	7.32	-2.47	2.68E-07
1419089_at	Mm.4871	Timp3	10.69	9.90	11.11	8.67	7.45	8.22	-2.45	1.13E-06
1424885_at	Mm.39723	Klhdc8a	8.35	7.89	8.70	6.27	5.32	6.22	-2.37	2.16E-07
1422520_at	Mm.390700	Nefm	7.91	8.01	8.45	5.49	5.88	6.03	-2.32	9.38E-09
1427183_at	Mm.44176	Efemp1	8.69	7.90	9.24	6.51	6.07	6.30	-2.31	4.38E-07
1435494_s_at	Mm.355327	Dsp	11.52	9.98	10.39	8.65	8.00	8.42	-2.27	2.67E-06
1448416_at	Mm.243085	Mgp	8.38	9.22	10.55	6.97	7.04	7.39	-2.25	2.78E-05
1435493_at	Mm.355327	Dsp	11.67	10.23	10.68	9.06	8.24	8.63	-2.22	3.15E-06
1420467_at	Mm.34201	Psors1c2	9.48	9.24	9.56	7.28	7.31	7.03	-2.22	3.22E-09
1434353_at	Mm.329991	Sfmbt2	10.39	9.86	9.99	8.74	7.60	7.28	-2.20	2.61E-06
1437967_at	Mm.26579	Ccdc141	8.08	8.22	7.70	6.42	6.00	5.01	-2.19	1.70E-06
1416242_at	Mm.224306	Klh13	10.01	9.91	9.83	8.02	7.81	7.34	-2.19	1.46E-08
1421144_at	Mm.21662	Rpgrip1	12.04	12.24	11.86	10.66	9.60	9.33	-2.18	1.19E-06
1449334_at	Mm.4871	Timp3	10.55	9.80	10.87	8.51	7.95	8.27	-2.16	4.10E-07
1424186_at	Mm.181074	Ccdc80	12.15	11.56	12.60	10.41	9.67	9.78	-2.15	6.37E-07
1424131_at	Mm.7562	Col6a3	10.57	10.64	11.45	9.59	8.17	8.54	-2.12	7.90E-06
1448169_at	Mm.22479	Krt18	10.38	8.64	8.43	7.12	7.00	7.01	-2.10	4.35E-05
1427492_at	Mm.34964	Pof1b	7.81	8.18	8.06	6.75	5.69	5.33	-2.09	2.79E-06
1415846_a_at	Mm.16563	Ldhc	6.74	6.52	5.92	4.60	4.17	4.19	-2.07	1.85E-07
1435420_at	Mm.333189	Slc4a5	6.49	6.83	5.80	4.53	4.57	3.81	-2.07	1.32E-06
1415824_at	Mm.479161	Scd2	7.98	8.37	8.17	6.14	6.18	6.07	-2.04	9.70E-09
1417210_at	Mm.250909	Eif2s3y	11.26	11.32	11.27	9.61	9.04	9.08	-2.04	2.98E-08
1433474_at	Mm.125580	Edil3	6.18	6.67	7.81	5.34	4.40	4.83	-2.03	2.56E-05
1426852_x_at	Mm.5167	Nov	8.38	7.79	8.53	6.41	5.83	6.38	-2.02	3.04E-07
1429274_at	Mm.41381	Lypd6b	7.73	7.87	7.65	5.67	5.66	5.90	-2.00	1.02E-08
1419729_at	Mm.134024	Tex11	5.18	5.00	4.79	6.82	7.13	7.01	2.00	1.92E-08
1449590_a_at	Mm.2045	Mras	7.21	7.25	7.07	9.10	9.33	9.16	2.02	8.42E-09
1419417_at	Mm.1402	Vegfc	8.05	7.74	7.87	10.12	9.85	9.79	2.03	1.28E-08
1424045_at	Mm.46654	5730437N04Rik	7.87	7.99	8.03	9.37	10.28	10.40	2.05	4.52E-07

1456768_a_at	Mm.272673	Mmrn2	6.11	6.26	6.26	8.38	8.20	8.21	2.05	5.81E-09
1448291_at	Mm.4406	Mmp9	6.44	5.80	5.89	8.51	7.92	7.88	2.06	2.16E-07
1440739_at	Mm.1402	Vegfc	7.73	7.45	7.48	9.87	9.61	9.36	2.06	1.92E-08
1429177_x_at	Mm.279103	Sox17	4.40	4.83	4.56	6.35	6.69	6.98	2.08	4.52E-08
1439759_x_at	Mm.45514	Sult6b1	5.16	5.15	4.92	6.80	6.80	7.89	2.09	8.23E-07
1460667_at	Mm.2548	U90926	8.23	7.41	7.83	10.17	9.07	10.54	2.10	7.37E-06
1417256_at	Mm.5022	Mmp13	9.34	9.21	10.76	12.32	11.26	12.06	2.11	2.70E-05
1436291_a_at	Mm.275974	Dpys	4.67	4.44	4.01	6.13	6.68	6.72	2.14	8.76E-08
1437479_x_at	Mm.219139	Tbx3	5.53	6.25	5.71	7.95	8.31	7.81	2.19	4.52E-08
1423232_at	Mm.5025	Etv4	7.02	7.08	7.14	9.44	9.43	8.96	2.20	6.10E-09
1452614_at	Mm.297245	Bcl2l15	6.50	5.32	5.64	7.62	7.39	9.08	2.21	2.99E-05
		Ifi203 ///								
1451567_a_at	Mm.472787	LOC100044071	4.08	4.50	4.58	7.27	6.07	6.53	2.23	4.21E-07
1423582_at	Mm.391208	Dmrt1	7.97	8.12	7.86	9.95	10.23	10.66	2.30	9.00E-09
1448029_at	Mm.219139	Tbx3	7.39	7.58	7.24	9.91	10.01	9.50	2.40	2.17E-09
1419728_at	Mm.4660	Cxcl5	7.59	7.82	8.49	10.73	9.57	10.84	2.41	1.03E-06
1449025_at	Mm.426079	Ifit3	5.81	5.64	5.88	8.35	8.45	8.03	2.50	6.82E-10
1418110_a_at	Mm.15105	Inpp5d	7.00	7.04	6.92	9.87	9.43	9.22	2.52	1.43E-09
1423555_a_at	Mm.30756	Ifi44	4.73	4.52	4.46	7.29	7.33	6.70	2.54	1.79E-09
1434528_at	Mm.24204	Aard	8.09	8.45	8.00	10.53	10.62	11.05	2.55	1.45E-09
1418837_at	Mm.26928	Qprt	6.42	6.53	6.59	8.80	9.28	9.11	2.55	4.88E-10
1451411_at	Mm.103439	Gprc5b	5.72	5.44	5.05	7.89	8.00	8.17	2.62	1.11E-09
1418395_at	Mm.100741	Slc47a1	6.36	6.60	6.32	9.03	8.98	9.16	2.63	1.50E-10
1438148_at	Mm.244289	Cxcl3	4.11	3.91	4.00	7.88	5.66	6.92	2.81	1.87E-06
1434917_at	Mm.22847	Cobl	7.89	7.96	7.61	10.87	10.92	10.12	2.82	1.43E-09
1450826_a_at	Mm.14277	Saa3	7.90	7.93	8.59	11.67	11.25	10.16	2.88	1.39E-07
1437019_at	Mm.27156	2200001I15Rik	9.31	9.14	8.53	11.46	12.09	12.15	2.91	2.15E-09
1439059_at	Mm.260106	Fam199x	4.06	4.11	3.93	7.31	6.83	7.09	3.04	2.98E-11
1420568_at	Mm.5171	Stra8	6.52	6.46	6.11	9.13	8.94	10.18	3.05	6.10E-09
1429377_at	Mm.479859	2410004A20Rik	6.36	6.86	6.39	9.62	10.12	9.45	3.19	1.17E-10
1456242_at	Mm.45676	Gm7325	9.54	9.49	8.46	12.47	12.68	12.66	3.44	3.40E-10
1425764_a_at	Mm.24210	Bcat2	6.22	6.01	5.73	9.15	9.83	9.63	3.54	1.72E-11
1443621_at	Mm.291131	Xaf1	5.22	5.05	5.04	9.17	8.96	7.97	3.60	2.39E-10
1418191_at	Mm.326911	Usp18	6.67	5.95	6.29	10.47	9.99	9.64	3.73	3.23E-11
1437054_x_at	Mm.42733	Prm1	3.51	3.40	3.49	7.48	7.80	7.07	3.98	1.08E-12
1418580_at	Mm.475107	Rtp4	7.09	6.99	7.29	11.45	11.21	10.82	4.04	8.23E-13
1439379_x_at	Mm.42733	Prm1	3.37	3.49	3.50	7.55	7.81	7.45	4.15	1.03E-13
1450783_at	Mm.439751	Ifit1	4.96	5.16	4.86	9.84	8.75	8.87	4.16	1.62E-11
1432198_at	---	---	4.54	4.69	4.58	8.80	8.93	8.89	4.28	5.04E-14